Impact of Climate Change on Regional and Global Biodiversity: a Meta-Analysis

by

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Declaration

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Abstract

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Peer-review publication has become a standard vessel for sharing the knowledge gained in scientific research, with its number increasing exponentially in the recent decades. To this end, robust statistical methods that allow us to synthesize and generalize these knowledge points in published literature, and to develop and test overarching hypotheses, are urgently needed. We here use a meta-analysis and test a few hypotheses on the influence of climate change on biodiversity maintenance in regional ecosystems. Based on the work by Hans van Houwelingen and colleagues in 2002, we developed a maximum likelihood estimate of parameter in random and mixed effect models. This approach was then applied to a real dataset collected from published literature of the impact of ambient temperature increase on species performance. We found that in general, the current and predicted temperature is negatively affecting different species independently of localities. Some taxonomic groups are negatively affected by temperature rise whilst others seem to be robust to the temperature change. Species richness and suitable habitat were found to be the most sensitive species attributes to temperature rise. We classified the methodology used by studies from which we extracted the data in two main groups: observation and modelling. We found that the modelling approach exaggerates the reality found from the observations. The main focus of this study was

to add another layer of knowledge on the loss of biodiversity due to climate change, thereby showing that if nothing is done to stabilize the increase of temperature, the current species taxa tolerant to a temperature rise will also be vulnerable, therefore more loss of biodiversity can be expected toward the end of this century.

Uittreksel

Impak van Klimaatsverandering op Streeks-en Globale Biodiversiteit: 'n Meta-Analise

("Impact of Climate Change on Regional and Global Biodiversity: a Meta-Analysis")

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Tesis: MSc

Desember 2012

Groeps-hersiening publikasies het 'n standaard vaartuig geword vir die deel van kennis wat in wetenskaplike navorsing versamel is, met die aantalwat eksponensieel toeneem in die afgelope dekades. Vir hierdie doel, is robuuste statistiese metodes wat toelaat dat ons sintetiseer en hierdie kennis punte veralgemeen in gepubliseerde literatuur, en oorkoepelende hipoteses te ontwikkel en te toets, dringend nodig. Ons gebruik hier 'n meta-analise en toets 'n paar hipoteses oor die invloed van klimaatsverandering op biodiversiteit onderhoud in plaaslike ekosisteme. Gebaseer op werk van Hans van Houwe Lingen en kollegas in 2002, het ons 'n maksimum waarskynlikheid beraming van die parameter in random en gemengde effek modelle ontwikkel. Hierdie benadering is dan toegepas op 'n ware datastel wat ingesamel is van gepubliseerde literatuur oor die impak van 'n toename van omgewingstemperatuur op spesie prestasie. Ons het gevind dat oor die algeheel, die huidige en voorspelde temperatuur verskillende spesies negatief beÃ¯nvloed onafhanklik van lokaliteite. Sommige taksonomiese groepe word negatief beÃ¯nvloed deur die temperatuur styg, terwyl ander robuust is teen die temperatuur verandering. Spesierykheid en geskikte habitat is bevind as die spesies eienskappe wat mees sensitief is vir temperatuur styg.

Ons het die metodologie wat gebruik word deur studies waar ons die data onttrek het geklassifiseer in twee hoofgroepe: waarneming en modellering. Ons het gevind dat die modellering benadering oordryf die realiteit van die waarnemings. Die hooffokus van hierdie studie was om nog 'n laag van kennis by te voeg wat bestaan uit die verlies van biodiversiteit as gevolg van klimaatsverandering, en daardeur bewys dat indien niks gedoen word om die verhoging van die temperatuur te stabiliseer nie, die huidige spesie taksa wat wys om te volhard teen die temperatuur aanleiding sal ook kwesbaar wees, dus meer verlies van biodiversiteit in die rigting van die einde van hierdie eeu.

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All thanks go to almighty God for allowing me the life which allows me the completion of the master's program. I would like to express my sincere gratitude to the following people for their contribution in the completion of this assignment

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Dedications

I dedicate this thesis to my late parents.

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Chapter 1

Introduction

1.1 Background information

The global climate has shown drastic changes in the last decades (e.g. increase in temperature) and is predicted to change even more in the coming decades as a result of natural cycle variability (e.g. increase in solar luminosity intensity) and human activities (e.g. deforestation, burning fossil fuel and mismanagement of CO_2 released from industries). Some regions will be more affected by climate change such as throughout the African continent, where it is predicted that the temperature will increase by $6.4°C$ between 1999 and 2100 [Leny *et al.*, 2007].

The impact of climate change on the biosphere has been discussed by different scholars [Menendez *et al.*, 2006; Ohlemueller *et al.*, 2008; Parton *et al.*, 1995]. Experimental studies and mathematical models (e.g. ecological niche modelling) have shown that the response of species to climate change follows different trends [Dormann and Woodin, 2002]. Ecological niche models correlate current species distribution to present climate conditions and, thereafter, project future change in species distributions (and thus species richness) under different scenarios of future climate change [Thuiller, 2003]. However, predictions from these models are often scale sensitive [Randin *et al.*, 2009] and topography sensitive [Luoto and Heikkinen, 2007]. It is, thus, crucial to compare model predictions with observations.

Given the increase of the current climate change, it becomes more relevant to understand how different species will respond to change in temperature and precipitation patterns once the climate change reaches a critical threshold at regional and global scales. Despite the extensive literature on biodiversity

loss due to climate change, a global picture has not yet been developed. The absence of such a review, undoubtedly, limits our ability to assess the conservation statues (e.g. vulnerability) of a species, community or the regional and global ecosystems.

To our knowledge, there is no study that encompasses the impact of climate change on species richness, suitable habitat, biomass and species abundance at the global scale across taxa using standardized methods such as meta-analysis [Borenstein *et al.*, 2009]. We thus propose to conduct a systematic meta-analysis of the regional and global potential impacts from changes in ambient temperature on species of different taxonomic groups.

1.2 The aim of the study

This project aims to investigate the effects of changes in ambient temperature around the world on species richness, suitable habitat, biomass and species abundance, and how different taxa respond to the recent and predicted changes in temperature, as well as whether predictions fit the observations using a meta-analysis approach.

1.3 Research objectives

- Collect data from published studies that address ambient temperature change impact on species richness, suitable habitat, biomass and species abundance,
- Determine an appropriate measure of the effect size,
- Apply the meta-analysis approach to tackle the research questions.

1.4 Research questions

As a way of investigating the impacts of temperature change on species using the meta-analysis approach and efficiently investigate the aim of this study, the following questions will be addressed:

- Does the effect size of the impact of temperature change on species richness significantly differ at small, medium and large geographical extent?

- Which taxonomic groups (e.g. Reptiles, angiosperms) are more vulnerable to the temperature rise?
- What are the most sensitive species' attributes to the change of temperature?
- Which regions are prone to the rise of temperature?
- What is the effect size of the temperature change impact on species at different altitude?
- Whether different models (e.g. ecological niche models) predict differently and whether they over or under estimate the observations?
- How dispersal capacity of species contributes to its response to temperature change?

1.5 Definitions

Definition 1. *Effect size, in general, is an index that measures the treatment effect [Borenstein et al., 2009]. In this study, the effect size reflects the strength of the relationship between introduction of disturbance parameter in an ecosystem and the response of the ecosystem. In other words, the effect size is defined as a value reflecting the effect of environment condition change on species. The effect size is the unit currency of meta-analysis.*

Definition 2. *A meta analysis is a quantitative approach wherein a set of statistical methods is used to summarize and synthesize the results from previous independent studies on a similar research question. If the studies are not homogeneous, the meta analytical approach provides a way of exploring the heterogeneity across studies [Vila et al., 2011].*

Before we can start applying the meta-analysis approach to draw inference from the data, a review of the literature on the impact of temperature change on biodiversity and description of data collection are needed. In chapter 2, we provide a review of literature pertaining to the species responses after temperature change.

Chapter 3 provides a detailed description of used methods to collect data. A description of used approaches to quantify the effect of temperature rise on biodiversity is then given.

In chapter 4, random and mixed effect models are applied to a real data base.

Chapter 5 draws together the pertinent findings of this study. We conclude this chapter by proposing future works in this area.

Chapter 2

Literature review

2.1 Introduction

In this chapter, we present some examples from the literature of the effects of climate change on insects, mammals, angiosperms, gymnosperms and amphibians among others. The focus on this classification is motivated by two reasons: first, plant growth form and plant functionality have often been used in meta-analysis to show the effect of temperature change but no study have used the aforementioned classification to provide the global picture of the effect of temperature change. Secondly, we want to know which taxonomic groups are more vulnerable to the rise of temperature.

2.2 Definition of climate change

Climate is the collection of statistics for long term temperature, precipitation, atmospheric particle count and other meteorological measurements in a given area [Field *et al.*, 2009]. According to Leny *et al.* [2007], climate change is defined as the change of the state of climate explained by significant statistical change of the mean and / or the variability of its statistics persisting for long period, normally from decades to millions of years, due to natural variability (e.g. solar activity, volcanoes) or as a result of human activities (e.g. emission of greenhouse gases). Climate change is reflected by changes in temperature, the shift in precipitation patterns [Yang *et al.*, 2011], increasing of CO_2 atmospheric concentration and enrichment of nitrogen [McClean *et al.*, 2011].

2.3 Greenhouse gase emission as a source of climate change

One of the main conclusions of the Intergovernmental Panel on Climate Change (IPCC) working group I's fourth assessment [IPCC, 2001] was that the increase of temperature since the middle of this century is due to an increase of greenhouse gases concentration resulting from human activities. Some of the gases are found or produced in the following manner:

- Carbon dioxide: This occupies a small part but an important greenhouse gase. Carbonate dioxide is released in processes such as respiration, volcano eruptions, deforestation and burning fossil fuel. Recently, the expansion of industries contributes the major portion of CO_2 released to the atmosphere.
- Nitrous oxide: This greenhouse gas is produced during agricultural activities such as the use of commercial and organic fertilizer.
- Methane: On the molecule basis, methane is more active than carbon dioxide but less abundant in the atmosphere than the latter. Methane is hydrocarbon gas produced by both natural sources and human activities such as decomposition of wastes and in agriculture.

The continuous accumulation of greenhouse gases will result in:

i An overall increase in ambient temperature on the Earth,

ii The resultant temperature increase affecting current suitable habitat of many species.

2.4 Predicted climate change scenarios

The current understanding of predicted climate change is based on General Circulation Models (e.g. HadCM3[1], CGCM2[2] and CSIRO2[3]). General Circulation Models (GCM) are mathematical models used in weather and climate

[1]HadCM3 is coupled GCM ocean-atmospheric developed by Hadley in UK and mainly used in IPCC [2001].

[2]CGCM2 is the second coupled GCM developed by Canadian Centre for Climate Modeling and Analysis.

[3]CSIRO2 is coupled GCM developed by CSIRO Marine and atmospheric Research.

change forecast at regional and global scales [IPCC, 2001]. Given the projection of climate change at the end of the 21^{st} century and the lack of knowledge about the impact of human activities, especially the quantity of greenhouse gases which will be introduced to the atmosphere in coming years, this increase the uncertainty about prone regions to temperature rise and species which could become vulnerable at the end of this century [Timothy *et al.*, 2004; Ohlemueller *et al.*, 2008; Maclean and Wilson, 2011].

As a way of understanding the future change of climate, its physical, economic and ecological impact, four socio-economic emission scenarios have been proposed by the IPCC [Leny *et al.*, 2007] which are:

The first scenario A1 describes a high impact on biosphere as a consequence of a rapid economic development. This would include an increase of population until 2050, followed thereafter by a decline and a rapid introduction of new technologies to the market where CO_2 atmospheric concentration is predicted to double from 380 parts per million (ppm) to 970 ppm and a global mean annual temperature increases of $4.5°C$.

The second scenario A2 describes a continuous economic development and population increase with a slower technological innovation and more fragmented than other climate change scenarios. According to this scenario, the CO_2 atmospheric concentration will increase from 380 ppm to 860 ppm between 2000 and 2100 with a global mean annual temperature predicted to increase by $3.8°C$.

The third scenario B1 and lowest climate change impact describes the introduction of clean efficient technology, rapid change towards service and information economy, increase of population until 2050, followed by a decline thereafter. The CO_2 atmospheric concentration between 2000 and 2100 is predicted to increase from 380 ppm to 530 ppm and the global mean annual temperature is predicted to increase by $2.0°C$.

The forth scenario B2 emphasizes on local solutions to economic, social and environmental sustainability. Population increase at lower rates, the CO_2 atmospheric concentration is predicted to increase from 380 ppm to 610 ppm and the global mean annual temperature is predicted to rise by $2.7°C$. In summary, human activities (e.g. CO_2 released from industries, deforestation) will contribute enormously to predicted climate change.

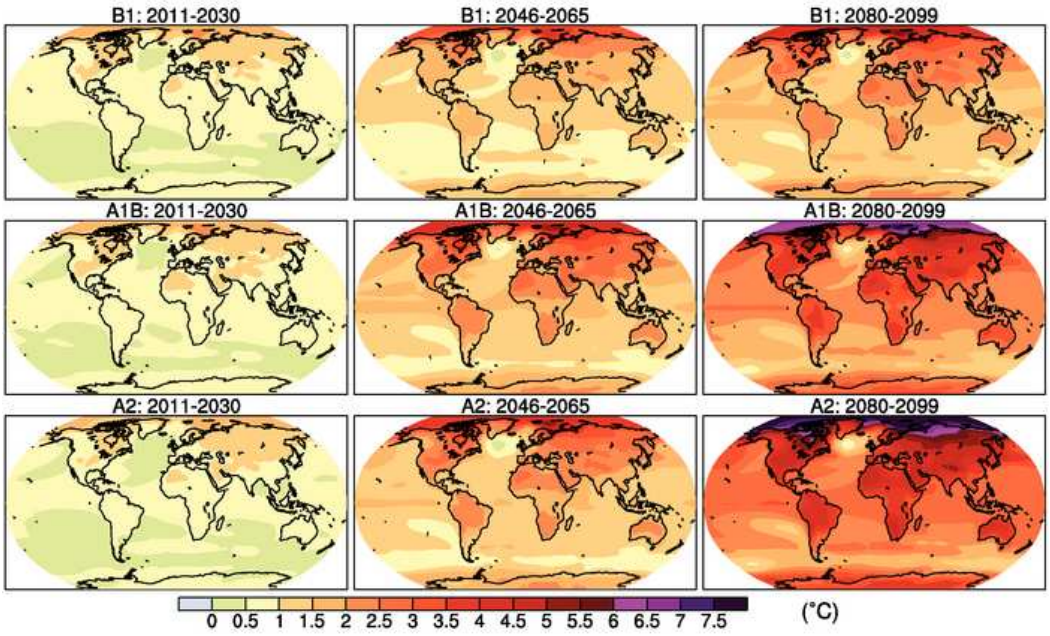

Figure 2.1: Regions prone to temperature rise according to the Intergovernmental Panel of Climate Change (IPCC) scenarios: B1 in the top, A1 in the middle and A2 in bottom versus three time intervals [IPCC, 2007*b*]

2.5 Temperature change effect on biodiversity

The global climate has shown evidence of change during the last decades. A few examples include the observed relative increase of temperatures, CO_2 atmospheric concentration, rising sea level and decreasing snow cover in the Northern hemisphere. The climate is predicted to change more in the coming decades as a result of natural cycle variability (e.g. increase in solar luminosity) and human activities such as deforestation, burning fossil fuel and mismanagement of CO_2 released from industries [IPCC, 2001]. Two major scenarios have been predicted using the general circulation model based on doubling the CO_2 concentration. Firstly, the global temperature is predicted to increase by 1.5 to $4.5°C$ [Cameron and Scheel, 2001]. Secondly, the increase will not be evenly distributed [Leny *et al.*, 2007; Lundquist *et al.*, 2011]. This will result in local

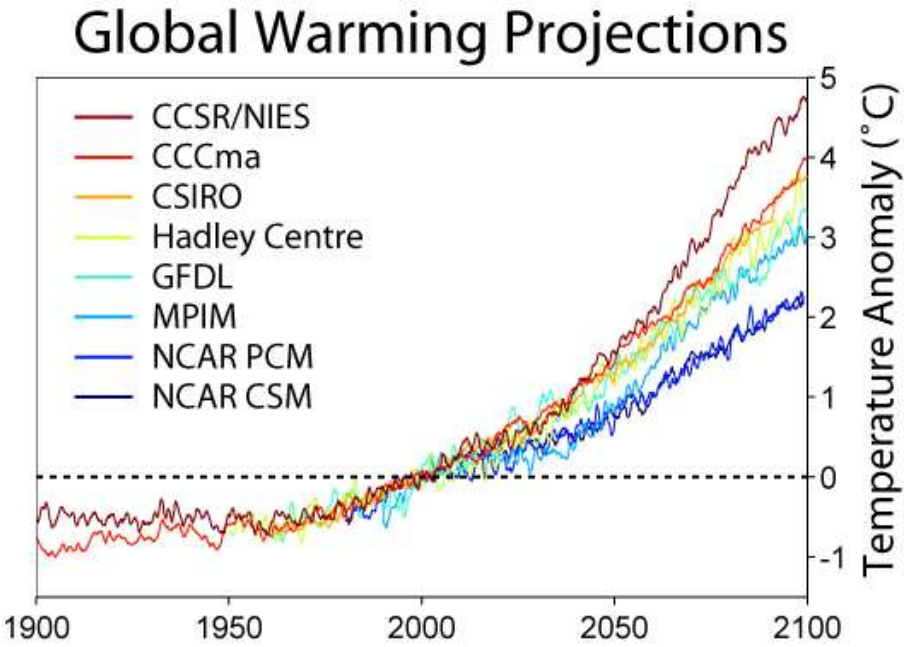

Figure 2.2: Predicted temperature increase at the end of the 21^{st} century relative to year 2000. Different lines represent the results of forecasted temperature rise from models developed by the Centre for Climate System Research (CCSR/NEIS), Canadian Centre for Climate Modelling and Analysis (CCCma), Commonwealth Scientific and industrial Research Organisation (CSIRO), Hadley Centre of UK meteorology Office, Fluid Dynamics laboratory (GFDL), Max Plank Institute for Mathematics (MPIM), National Centre for Atmospheric Research: Parallel Climate Model (NCAR PCM) and National Centre for Atmospheric Research: Climate System model (NCAR CSM) respectively.

environmental (temperature and precipitation) variability [Pompe *et al.*, 2008; Yang *et al.*, 2011; McClean *et al.*, 2011] with some regions being more affected than others [IPCC, 2007*a*]. For example, across the African continent, the temperature is predicted to increase by up to $6.4°C$ between 1999 and 2100 [Leny *et al.*, 2007] while only a $2.1°C$ increase is predicted for New Zealand [Lundquist *et al.*, 2011]. These changes are, however, not yet fully understood in terms of the effects on local and global biodiversity. Understanding the responses of species to climate change would give a broad idea if the predicted environmental conditions are a threat to biodiversity.

The growing number of evidence from model projections [Calef *et al.*, 2005], observations of species response to climate change [Yang *et al.*, 2011], and meta-analysis of the impact of climate change have shown that predicted trend of species response to climate change will mainly be driven by temperature rise

[Dormann and Woodin, 2002]. The impact of temperature change will be enforced by indirect effects such as land use, species competition and predation. Different organisms, however, have shown to respond individually to change of temperature [Thuiller *et al.*, 2005]. The effects of temperature rise are pronounced as follows: (i) upward shift of suitable habitat, (ii) species richness change and (iii) suitable habitat contraction.

Understanding how species distribution and diversity will respond to climate change is important for ecologists and conservationists. This is due to the fact that species are responding individually and the gap of vulnerable species taxa to the change of temperature. The overall abundance and suitable habitat would be negatively affected [Dormann and Woodin, 2002; Luoto and Heikkinen, 2007]. The species suitable habitat is expected to decline globally. However, local species suitable habitat may increase or decline [Malcolm *et al.*, 2006]. For example, a temperature increase has shown an enhanced effect on butterfly species richness with wide spread species (generalists) greater than species confined to a local area (specialists), despite the individual abundance decline. This increase of temperature also increased the female size resulting in the increase of fecundity and population growth rate. However, the winter temperatures can affect negatively the growth rate of the butterflies [Matter *et al.*, 2011]. The negative impact on the butterflies was suggested to be an indirect effect in the phenology of their host plant species in response to changes in temperature. The phenology change in host plants is done by producing a defensive chemical substance affecting the larvae development [Menendez *et al.*, 2006].

Plant communities also have different responses to climate change. One example is the white spruce, thought to be limited by moisture with an increase over the critical value of $2°C$. On the other hand, the range of deciduous forest may expand with an increase in temperature and precipitation [Calef *et al.*, 2005]. Tundra is expected to be replaced by forests under a predicted temperature increase of $6°C$ within a lag of 80 years while tundra may expand their potential range under the increase of precipitation compared to the current conditions [Starfield and Chapin, 1996]. Further, the overall increase in CO_2 concentration in grassland ecosystems under or without simulation of the current climate change conditions increases plant production, abiotic decomposition rate and soil organic carbon storage [Parton *et al.*, 1995]. Parton *et al.* [1995] showed that this effect of CO_2 reduces the production loss in grassland

ecosystems by 60%.

In general, 20 to 30% of species are predicted to be extinct if the temperature increase is beyond the threshold value of 2 to 3°C [Leny *et al.*, 2007]. The mammal species in different regions are also negatively affected by climate change. For example, chimpanzees and gorillas in Africa are predicted to lose up to 10 and 75%, respectively, of their suitable habitat and their population density is predicted to decline by 30% for all species by 2100 [Lehmann *et al.*, 2010]. The bird community is predicted to be sensitive to changes in temperature and precipitation by shifting their habitat northward and upward in elevation [Araújo *et al.*, 2011]. The bird species breeding in high elevation habitats, for example in Europe, will be strongly negatively affected by precipitation increase than in low land [Li *et al.*, 2009]. Rodenhouse *et al.* [2008] showed that an increment of 2°C will result in loss of more than half of the bird community habitat in high elevations. Therefore, given the projected temperature increase, we may speculate that all bird communities in high elevated habitats will be extinct towards the end of this century [Lemoine *et al.*, 2007]. Precipitation variability may impact bird breeding productivity by changing their arrival and migration timing [Rodenhouse *et al.*, 2008]. In this regard, the long-distance dispersal will be more negatively affected than short-distance dispersal while resident bird species may cope with changing climatic conditions [Lemoine *et al.*, 2007]. However, there is a controversy regarding migrant bird communities depending of the study area [Kolecek *et al.*, 2010]. The bird species in urban areas are less affected by warmer conditions than rural species [Rodenhouse *et al.*, 2008]. Given the numerous evidence, we predict that a global increase in temperature will in overall affects plant and animal communities negatively. A survey is thus needed to assess if studies conducted at different spatial scales give comparable results, and whether the consistence of predicted species distribution is robust.

Despite the effort in predicting the impact of climate change on biodiversity, we are uncertain to what extent such impacts will occur wonder. Menendez *et al.* [2006] showed that more than a half of the predicted impact of precipitation and moisture in 1962 did not take place in 1990. This may be explained by the omission of factors which are sensitive to species. For example, Luoto and Heikkinen [2007] showed that inclusion of topography heterogeneity increased the accuracy in predictions.

If there is nothing done to reduce the greenhouse gases, in general, species

are expected to decline because they are not able to adapt to new conditions of climate change or even able to disperse due to geographical and physical boundaries to search for suitable habitat [Burgmer and Hillebrand, 2011].

2.6 Quantification of climate change

The quantification of the impact of climate change on biodiversity has been done in various ways by many empirical and non-empirical studies using observation experiments. On the other hand, mathematical and statistical modelling techniques are used to understand the response of species to the change of ambient temperature [Thuiller *et al.*, 2005].

Among them, we have General Linear model (GLM) and General Additive Model (GAM) which are the most used. Other alternative methods of assessing future distribution have recently been introduced. These methods include Classification and Regression Tree Analysis (CART) and Artificial Neural Networks (ANN) [Brotons *et al.*, 2004].

Ecologists have observed that different models give different results for the same species and different methods tend to vary across species. That is why BIOMOD has been introduced [Thuiller *et al.*, 2005]. This approach maximizes the spatial distribution accuracy of species by using different approaches from parametric (GLM, GAM) to non-parametric (CART, ANN) from predicting species richness and distribution. We choose either the best accuracy method (model) to predict species distribution or keep all methods and then compare their results. As a way of verifying the fit of these models, two methods are currently used in ecology. Either the dataset is divided into two subsets where one subset (in general 70%) is used to calibrate the model, and the other part is used to evaluate the model projection, or the current projection of species distribution are compared to long term observation of the effect of climate change on species [Brotons *et al.*, 2004].

The models used to predict future distribution of species have some weakness and advantages. GLM are the most common used with its ability to predict current distribution, however, the inability of dealing with complex response curves have made ecologists use GAM to describe the hierarchical interaction between species and its accuracy to predict current potential distributions. ANN which are continuously used but limited by the inability to identify the causal relationships from the network structure made them

weak. However, the power of ANN to deal with non-normal variable and their accuracy to predict the environment envelopes which have non-linear relationship with the environment variables make them useful [Thuiller *et al.*, 2005]. The uncertainty of the aforementioned models makes it difficult to understand the sensitivity between species and predicted climate change scenarios. Three sources of uncertainty are: (*i*) the uncertainty based on predicted greenhouse gas emission, (*ii*), the uncertainty due to the choice of modeling technique and (*iii*) the uncertainty due the threshold value to transform probability in presence-absence form [Thuiller, 2003].

In summary, the reliability of future potential distribution of species depend on the models used, where small differences in evaluation process may result in large difference in projected impact of climate change [Thuiller, 2003].

Chapter 3

Methodology

3.1 Introduction

As a way of understanding current and predicted general trend of the impact of ambient temperature change, the meta-analysis approach throughout independent studies will be selected. The use of this approach was motivated by three reasons.

- It considers the weight of each study included in the review.
- The meta-analysis approach attributes significant heterogeneity to different defined moderators (e.g.methodology, study period).
- This approach helps to test overreaching ecological hypothesis.

Therefore, the meta-analysis approach, which is a powerful and informative statistical tool to synthesize and compare the results from different independent studies testing the same hypothesis will be used [Harrison, 2011].

Along this chapter, a detailed description of literature search and data extraction will be given. The three basic models of meta-analysis; fixed, random and mixed models; will be described. The methods to assess the heterogeneity and publication bias will be discussed. The study level variables (moderators) will be defined. We will conclude this chapter with the sensitivity analysis methods in meta-analysis which will be used to assess the robustness of the conclusions and provide the limitation of the meta-analysis approach.

3.2 Literature search and inclusion criteria

Normally, the data used in meta-analysis are extracted from published and no published literature. In this study, we only considered data from published literature. In the process of gathering evidence from the literature, we included studies without limitation based on any interval of time or specific localities. We looked for relevant literature in the Web of Knowledge using terms defined in Table 3.1. We did not consider meta-analysis, reviews and theoretical studies in our data set. We did however, consider articles cited in meta-analysis. Some articles were included more than once, as they have tested the effect of ambient temperature on several species. For articles that tested the effect of temperature on different intervals of time, we decide whether we would consider each case as independent or present the average of all cases.response, we decided to consider only published articles.

Table 3.1: Combination of terms used for the literature search

Database	Conjunction	Terms for literature search	Outcome
Web of Knowledge	OR AND	Biodiversity Species richness Climate change	327

In order to avoid bias related to the studies that may not be returned by the Web of Knowledge, we screened reference lists of collected literature for papers assessing the impact of temperature change on biodiversity. We considered observation and simulated studies with one or more replicates. On the other hand, for studies treating the effect of temperature change on more than one species, each case was entered independently. This may create a pseudo-replication in the meta-analysis approach, but the same methodology has previously been used successfully [Vila *et al.*, 2011].

For studies testing the effect at different times, each case was considered independently because the species response is dependent on time. Only studies with focus on animals and plants performance after climate change effect were considered. We did not limit the literature search to any locality or interval of time. We selected studies from which the performance of species after ambient temperature change could be quantified or was possible to compute from the presented data.

3.2.1 Data extraction

Using the defined terms in Table 3.1 in the procedure of searching for the literature, we recorded 327 articles after removing duplicates. After applying all aforementioned criteria, we found 99 eligible articles to be included in the meta analysis. From these eligible articles, we extracted 2077 independent cases included in our database (see Appendix A). For each case, we extracted either the mean, standard deviation (SD) and the sample size or the ratio of change and sample size. Some studies reported a correlation coefficient or a linear regression model. For the linear regression model, the tracing method was used to determine the correlation coefficient [Quinn and Keough, 2002]. As discussed by Borenstein *et al.* [2009], the correlation coefficient is considered as a measure of effect size.

3.3 Effect size computation

We calculated the effect size as a measure of the impact of climate change on biodiversity. As discussed by Borenstein *et al.* [2009]; DeCoster [2012], three categories of data were counted during data collection: continuous data, correlation data and binary data. Each category of data reported the mean, correlation coefficient and ratio respectively as a measure of effect size. Given the scale variability on measures collected, we defined "Log response ratio (R)" as a standardized measure of the reported effect sizes. The new measure R was used for further analysis.

Different mathematical procedure and conversion equations as shown in Section 3.4, were used depending on the data category presented by each study.

The notion of Log transformation in the measure R was introduced to standardize the distribution (variance) of the effect size computed from each category, since for some cases we dealt with small sample size [Kirkwood, 2003]. We excluded the cases of colonization and extinction because they were not supported by R.

3.4 Conversion among effect size

In this Section, we provide the statistical formula used to convert the effect size and their corresponding variance to R scale as illustrated in Figure 3.1.

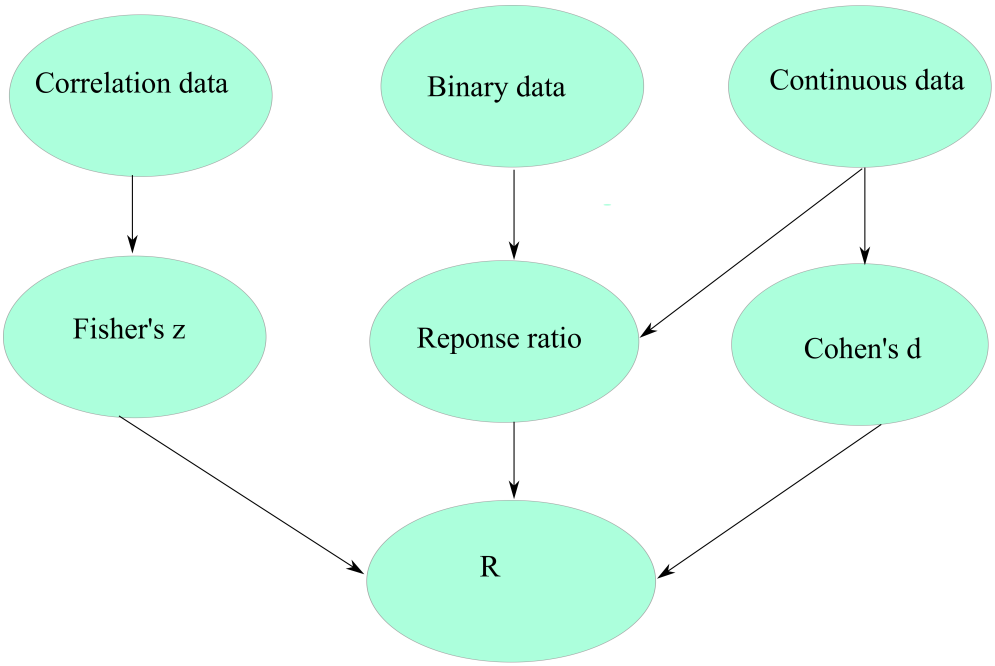

Figure 3.1: Transformation of the collected effect size from continuous, binary and correlation data to the standardized measure of the effect size R. Cohen's d stands for the standardized mean difference.

3.4.1 Converting from continuous data to R

3.4.1.1 Standard mean difference

Let's consider a i^{th} study that considers the effect of disturbance parameter (e.g. temperature) at time t_0 (initial time of study) and t_T (the end length time of the study). Let μ_0 and τ_0 be the mean estimate and standard deviation at initial time t_0 and μ_T and τ_T be the mean estimate and standard deviation at time t_T of disturbance parameter. We estimated the standardized mean difference (or the Cohen's d) as:

$$d = \frac{\mu_0 - \mu_T}{S_{within}}, \tag{3.4.1}$$

where S_{within} is the within standard deviation.
Let's us make the assumption that $\tau_0 = \tau_T$, which allows us to pool the standard deviation between groups. The reasons for pooling the standard deviation is that even if the identical variance between groups holds, they are unlikely to be equal in practice. Therefore, the within groups standard deviation was estimated as follow:

$$S_{within} = \sqrt{\frac{(n_0 - 1)\tau_0 + (n_T - 1)\tau_T}{n_0 + n_T - 2}}, \tag{3.4.2}$$

where n_0 and n_T stands for sample size at the beginning and end of the interval time.
The variance of Cohen's d is approximately estimated by

$$V_d = \frac{n_0 + n_T}{n_0 n_T} + \frac{d^2}{2(n_0 + n_T)}. \tag{3.4.3}$$

In the Equation (3.4.3), the first term stands for the uncertainty in estimation of Cohen's d and the second term reflects the uncertainty in estimation of the within standard error [Borenstein *et al.*, 2009].

3.4.1.2 Converting from d to g

The Cohen's d is slightly biased by overestimating the effect size in cases where the sample size is small. In 1981, Hedges proposed a collector factor J that yields the unbiased estimate of d [Hedges, 1981]. The mathematical formula for the collector factor J is given by

$$J = 1 - \frac{3}{4df - 1}, \tag{3.4.4}$$

where df represents the degree of freedom, which is estimated by $n_0 + n_T - 2$ for two independent groups. Therefore, the unbiased estimate of the effect size is given by Hedges's g as follow:

$$g = J \times d, \tag{3.4.5}$$

The variance for the unbiased estimate for the effect size (g) is given by

$$V_g = J^2 \times d. \tag{3.4.6}$$

3.4.1.3 Converting from g to R

As aforementioned, the purpose when computing the effect size is to generate a standardized measure which is R.
The transformation from g to R was carried out using the following equation

$$R = g \times \frac{\pi}{\sqrt{3}} \tag{3.4.7}$$

The conversion from the variance estimate of g to the variance estimate of R was done using the following equation

$$V_R = V_g \times \frac{\pi^2}{3}. \tag{3.4.8}$$

3.4.2 Converting from correlation data to R

3.4.2.1 Effect size based on correlational data

In the process of collecting data, some studies reported the correlation coefficient between two continuous variables (e.g. temperature and species richness) or a linear regression model. The coefficient correlation r can then be used as the effect size index. The variance of the correlation coefficient is then approximately given by

$$V_r = \frac{(1-r^2)}{n-1}, \tag{3.4.9}$$

where n reflects the sample size.
Furthermore, Borenstein *et al.* [2009] showed that the correlation coefficient is a biased measure of effect size since it is strongly correlated to its variance. That is why an unbiased estimate is obtained by converting correlation coefficient to the Fisher's z scale which is given by

$$z = \frac{1}{2} ln \left(\frac{1+r}{1-r} \right), \tag{3.4.10}$$

The variance of Fisher's z is thus estimated by

$$V_z = \frac{1}{n-3}. \tag{3.4.11}$$

3.4.2.2 Converting r to R

In the process of using the same standardized measure for all collected effect size, we converted the correlation coefficient and its estimate of variance to the Log response ratio scale. The Fisher's z was converted to R using the equation

$$R = \frac{2z}{\sqrt{1-z^2}} \times J \times \frac{\pi}{\sqrt{3}}, \tag{3.4.12}$$

The variance estimate of the Fisher's z was converted as follow

$$V_R = \frac{4V_z}{(1-z^2)^3} \times J^2 \times \frac{\pi^2}{3}. \tag{3.4.13}$$

3.4.3 Converting from binary data to R

The study outcomes are measured on physical scale where the outcomes are unlikely to be zero. The ratio of the means can be used as the estimate of the effect size index.

In order to stabilize the variance, the ratio (R) of means was log transformed. Therefore, we have the following expression

$$\log(R) = \log\left(\frac{\mu_0}{\mu_T}\right), \tag{3.4.14}$$

The variance for log ratio is then given by

$$V_{\log(R)} = S^2_{within}\sqrt{\frac{1}{n_0\mu_0^2} + \frac{1}{n_T{\mu_T}^2}}. \tag{3.4.15}$$

3.5 Meta-analysis models

3.5.1 Fixed effect size model

Assuming $i = 1, 2, \ldots, k$ independent studies with their corresponding observed effect size. Each estimate of effect size corresponds to the true effect size (R) plus the sampling error (ε). Note that if the sample size of the i^{th} study is infinitely large, the sampling error is approximately zero, therefore the observed effect size $(\hat{R})$ is equal to true effect size R. For example, for a study i, we can write that

$$\hat{R}_i = R_i + \varepsilon_i, \tag{3.5.1}$$

where R_i stands for the unknown true effect size for the i^{th} study, $\hat{R}_i$ and ε_i stand for the observed effect size and sampling error, respectively. The sampling error is assumed to be normally distributed with mean zero and known variance v_i. Therefore, the $\hat{R}_i$ is an unbiased estimate of the effect size and is normally distributed. In practice, the effect size is estimated from continuous data, correlation data and binary data as shown in previous Section 3.4.

Contrary to other general processes in statistics where we start with populations and make estimation about observed measures, in meta-analysis we work backwards. Meta analysis starts with observed measures and make overreaching hypothesis about populations. In order to estimate the overall effect size, we calculated an overall weighted mean of observed effects (see below).

3.5.1.1 The likehood estimate of the overall mean under fixed effect model

As discussed by van Houwelingen *et al.* [2002], the fundamental situation in meta analysis is that we deal with k studies in which the parameter of interest is $R_i (i = 1, 2, \ldots, k)$. However, all studies report $\hat{R}_i$ and standard error S_i. We assume that $\hat{R}_i$ extracted from independent random sample is a normally distribution with unknown mean R_i and known standard deviation S_i. Therefore, we can write that

$$\hat{R}_i \sim N(R_i, S_i), \tag{3.5.2}$$

Furthermore, it should be highlighted that it is not the normality of the frequency distribution of $\hat{R}_i$ that is employed in our analysis. Since this approach is likehood based, we use the likehood of the unknown parameter in each study which looks like the likehood of Equation (3.5.2). Therefore, for the i^{th} study, we can write the normality distribution function (F) as

$$F(R_i) = \frac{1}{\sqrt{2\pi S_i^2}} \exp\left[-\frac{1}{2S_i^2}\left(\hat{R}_i - R_i\right)^2\right], \tag{3.5.3}$$

However, the fixed effect model under the homogeneity makes the assumption that the between studies variance is null. Therefore, we can write that $R_1 = R_2 = \cdots = R_k = R$. Then the likehood function for the function $F(R)$ is given by

$$\rho(F(R)) = \prod_{i=1}^{k} F(R_i, R), \tag{3.5.4}$$

Since the Log function is a monotonic function [Wikipedia, 2004] , it is more convenient to use it for simplicity. Therefore, we have the following relation

$$\log(\rho(F(R))) = \sum_{i=1}^{k} F(R_i, R) = -\frac{1}{2}\sum_{i=1}^{k} \frac{(\hat{R}_i - R)^2}{S_i^2} + \log(2\pi) + \log(S_i^2), \tag{3.5.5}$$

Making the first degree derivative of the Equation (3.5.5), and find the maximization of it, we have the following maximum likehood estimate

$$\hat{R} = \frac{\sum_{i=1}^{k} \frac{\hat{R}_i}{S_i^2}}{\sum_{i}^{k} \frac{1}{S_i^2}}, \tag{3.5.6}$$

With the standard error of the maximum likehood estimate of the overall weighted effect size under fixed effect model

$$SE(\hat{R}) = \frac{1}{\sqrt{\sum_{i=1}^{k} \left(\frac{1}{S_i^2}\right)}}. \tag{3.5.7}$$

Definition 3. *The weight of each study in meta analysis, noted ω_i, under the fixed effect model is defined as the inverse of the within study variance.*

Applying the Definition 3 to the Equation (3.5.6) and Equation (3.5.7), these equations can be written as follow

$$\hat{R} = \frac{\sum_{i=1}^{k} \hat{R}_i \omega_i}{\sum_{i=1} \omega_i} \tag{3.5.8}$$

$$SE(\hat{R}) = \frac{1}{\sqrt{\sum_{i=1}^{k} \omega_i^2}} \tag{3.5.9}$$

Assuming that $\hat{R}$ is normally distributed, we can write the 95% confidence interval for the overall weighted mean which is given by

$$\begin{aligned} l.b_{\hat{R}} &= \hat{R} - 1.96 \times SE(\hat{R}) \\ u.b_{\hat{R}} &= \hat{R} + 1.96 \times SE(\hat{R}) \end{aligned} \tag{3.5.10}$$

On other hand, the test of statistical significance of the $\hat{R}$ is essential. Therefore, a Z score value is computed to test the null hypothesis ($H_O : \hat{R} = 0$) by

$$Z = \frac{\hat{R}}{SE(\hat{R})} \tag{3.5.11}$$

Note that there is a perfect relationship between confidence interval and P-value, which means that the confidence interval does not overlap the null value when the P-value for Z is less than 0.05.

3.6 Random effect model

In this section, we develop the inference of one of the basic models in meta analysis called the random effect model. The "random" term is explained by the fact that under this model, we assume that the true effect size vary between studies. In other words, the between studies variance is not null. The sources of heterogeneity are

i) The within study variance S_i^2

ii) The between study true variance τ^2

Therefore, if we suppose that $R_i^*(i = 1, \ldots, k)$ represents the true effect size and $\hat{R}_i^*(i = 1, \ldots, k)$ represents the observed effect size, we can write that

$$\hat{R}_i^* = R_i^* + S(S_i^2) + S(\tau^2) \tag{3.6.1}$$

3.7 Maximum likehood estimate under the random effect model

When conducting a meta-analysis from independent studies, the assumption of heterogeneity is questionable. This means that heterogeneity might be present and should be considered in the analysis if the test for heterogeneity is statistically significant.
The random effect model assumes that $\hat{R}_i^*$ is normally distributed with unknown mean and known variance considering the two sources for heterogeneity. Therefore, we can write that

$$\hat{R}_i^* \sim N(R^*, S_i^2 + H^2), \tag{3.7.1}$$

Using the techniques developed in previous paragraphs and from the assumption in Equation (3.7.1), the maximum likehood estimate of the overall of effect size under the random effect model is given by

$$\hat{R}^* = \frac{\sum_i^k \dfrac{R_i}{(S_i^2 + H^2)}}{\sum_{i=1}^k \dfrac{1}{(S_i^2 + H^2)}}, \tag{3.7.2}$$

The standard error estimate of the weighted mean log response ratio is given by

$$SE(\hat{R}^*) = \frac{1}{\sum_{i=1}^{k} \frac{1}{S_i^2 + H^2}}. \tag{3.7.3}$$

Definition 4. *The weight of each study in meta analysis under random effect model, noted ω_i^*, is defined as the inverse of the sum of the within study variance and between studies variance*

As a consequence of the Definition 4, we can write that

$$\hat{R}^* = \frac{\sum_i^k R_i \omega_i^*}{\sum_i^k \omega_i^*}, \tag{3.7.4}$$

with corresponding standard error

$$SE(\hat{R}^*) = \frac{1}{\sum_{i=1}^{k} \omega_i^*}. \tag{3.7.5}$$

3.7.1 Evidence of heterogeneity

Many estimators have been proposed to estimate the true between studies heterogeneity (τ^2), from Hunter-Schmidt to the empirical Bayes estimator. Among these estimators, one has been commonly used in meta analysis in estimating (τ^2) which is the method of moment or Dersimonian and Laird method. As described by Duval and Tweedie [2000]; Borenstein *et al.* [2009], We first computed the total heterogeneity (Q) defined as a sum of weighted squared deviation of each observed effect size from the overall weighted mean [Borenstein *et al.*, 2009]. Secondly, we determined the expected value of (Q) assuming that all studies share the same effect size (df) and finally we computed C which is a parameter helping to return to the original metric. Thus, we have the following equation

$$Q = \sum_{i=1}^{k} \omega_i^* (R_i - R)^2, \tag{3.7.6}$$

The Equation (3.7.6) shows that Q is a standardized sum square which is affected by the effect size. From the Equation (3.7.6), we can write the

following expression

$$Q = \sum_{i=1}^{k} \omega_i^* R_i^2 - \frac{\sum_{i=1}^{k} \omega_i^* R_i}{\sum_{i=1}^{k} (\omega_i^*)^2}, \tag{3.7.7}$$

On the other hand, the expected value of Q when assuming the studies to share the same effect size is given by

$$df = k - 1, \tag{3.7.8}$$

where k is the number of studies and the parameter C is given by

$$C = \sum_{i=1}^{k} \omega_i - \frac{\sum_{i=1}^{k} (\omega_i^*)^2}{\sum_{i=1}^{k} \omega_i}, \tag{3.7.9}$$

Let's us note the estimate of between studies heterogeneity by H^2, and it is given by

$$H^2 = \frac{Q - df}{C}. \tag{3.7.10}$$

The meaning of this variable is that if we were able to estimate the overall effect size from the true Log response ratio, then τ^2 will be the variance of the overall mean. This means that the H^2 is the observed between studies variance.

Furthermore, since some part of the total heterogeneity is random, it becomes more interesting to determine the proportion of the real heterogeneity across the observed estimate. Heggin proposed the statistic I^2 for real proportion of heterogeneity as follow [Borenstein *et al.*, 2009]

$$I^2 = \left(\frac{Q - df}{Q} \right) \tag{3.7.11}$$

3.8 Meta-regression

In case of significant heterogeneity between studies, it raises the question to explore the causes or the source of heterogeneity [Borenstein *et al.*, 2009]. In case of meta analysis, that can be done by analysis of covariates on case study level which could explain the difference between studies. In this regard, the meta-regression or mixed effect model has been discussed by different peer review articles as a way of attributing the heterogeneity to independent variables. In this section, we will limit on the assumptions and the formation of the model.

In the work of Verbeke and Lesaffre [1997] found that the heterogeneity was partially explained by initial measures and concluded that in the process of investigating the heterogeneity, we could check whether the independent variables are not associated with an initial measure which leads to multivariate regression with a two dimension outcome. However, in this study, we will limit on multi-dimension regression with one dimension outcome due to the limitation in data collection process. In this study, we have 8 covariates available: study location, year of study, species classification, species sub-classification, study geographic grid size, elevation range, biodiversity measures and species dispersal capacity.

3.8.0.1 Formation and assumption of the model

Let X_i stand for the row vector of covariates of study i,meta analysis relates the true Log response ratio R_i to the matrix of predictors $X_i\beta$ where β stands for a vector of regression coefficients. This relation is not perfect, there exits some residual heterogeneity which are modelled by a normal distribution. Thus we can write that

$$R_i \sim N(X_i\beta, \sigma), \tag{3.8.1}$$

However, taking into account the imprecision in the observed Log response ratio, the marginal approximate model is given by

$$\hat{R}_i \sim (X_i\beta, \sigma + S_i^2). \tag{3.8.2}$$

In summary, in this chapter we focused on the procedures used to collect data. We presented the commonly used models in meta-analysis and estimated their corresponding parameters using the maximum likehood approach. In the following chapter, we tested some ecological hypotheses using inference developed in this chapter.

Chapter 4

Data analysis and interpretation

4.1 Introduction

Before applying the inference defined in the previous chapter, Harrison and colleagues in 2011 defined the main points to tackle when doing a meta analysis as follow. Defining the distribution of the data, test for the heterogeneity between studies and attribute the significant heterogeneity to the defined moderators [Harrison, 2011]. In the following section, we will handle each point.

4.2 Descriptive statistics for our meta database

We collected data over 99 published articles (see Appendix A) from which after applying the defined criteria, 2084 cases were extracted. Each effect size reported by each case was converted to the Log response ratio (R) scale. However, as discussed by DeCoster [2012], the analysis of covariate requires that the studies report simultaneously R and the standard deviation. However, not all cases have done so. Over 2084, only 1466 reported the effect size and the standard deviation, equivalent to 70.2% of cases extracted from the published literature. Cases of animal species reported in our data set are equivalent to 333 (22.7%) and plants species equivalent to 927 (63.2%). After classification of all species in categories, algae was represented by one case, amphibians by 53 cases, angiosperms by 303, birds by 207 cases, insects by 236 cases, ferns by 2 cases, fungi by 65 cases, gymnosperms by 64 cases, mammals by 28 cases, reptiles by 51 cases and mosses were represented by 82 cases.
Considering the methodology used, observational cases represented 510 (24%)

Table 4.1: Number of cases extracted from published articles. Eurosia stands for studies simultaneously carried out in Europe and Asia

Location	Number of cases
Africa	154
Australia	68
Asia	48
North America	930
South America	121
Eurasia	63
Europe, Asia and Africa	4
Antarctica	4
Antarctic Ocean	1
Indian Ocean	3
Pacific Ocean	18
World	22

cases and simulation represented 1567 (75.1%). Within simulation category, all models were not evenly represented (more details see Appendix B.1). On the other hand, considering the inclusion of the lost and gain simultaneously in the computation process of the effect size, only 304 (15%) cases did consider it and 1051 (51%) did not.

4.3 Distribution of data and test for normality

Considering the remaining 1466 cases, given the assumption that our sample was a random sample from a population of normally distributed effect size, we fitted the distribution of Log response ratio with a normal distribution function as shown in Figure 4.1.

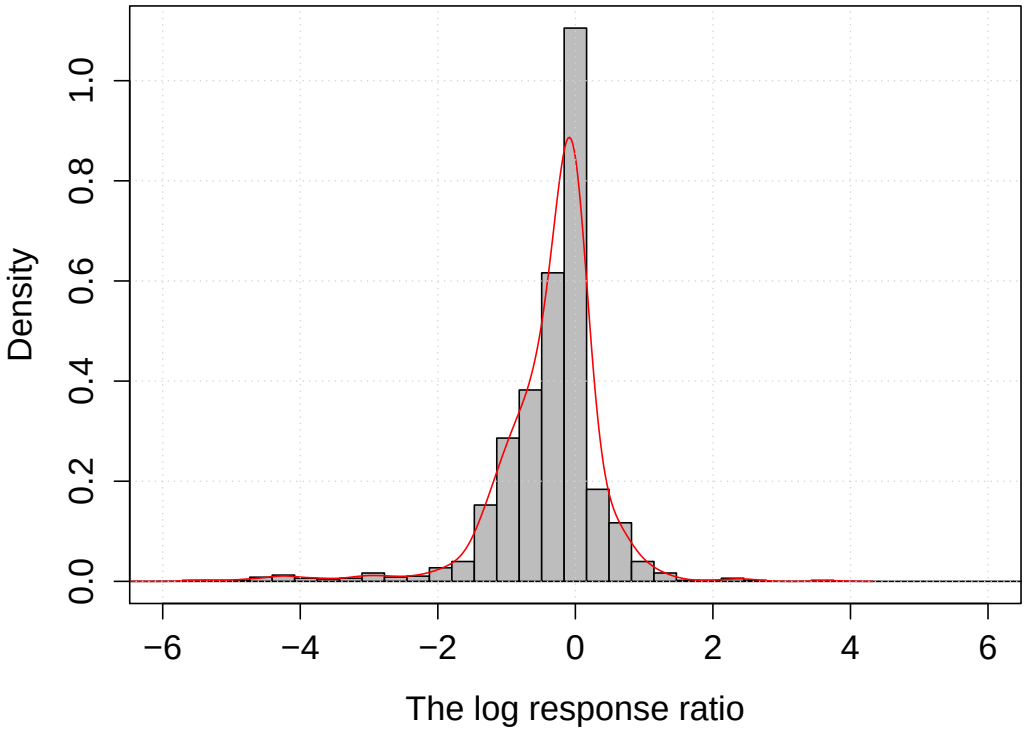

Figure 4.1: Frequency distribution of the effect size

Using Shapiro test in order to assess the normality of our sample size, shows that our sample was not normally distributed ($w = 0.8012, P < 0.0001$). Note that this test of normality is very strong and raises the question of mis-specification of the distribution. Verbeke and Lesaffre [1997] have shown that, in the general linear mixed models, the fixed parameters as well as the covariance parameters are still consistently estimated when the distribution of the random effects is mis-specified, as long as the covariance structure is correct. Thus our approach yields (asymptotically) unbiased estimate of the slope of the regression line even if the normal distribution assumption is not fulfilled.

4.4 Pseudo replication test

To test the pseudo-replication, we randomly selected one case for each study and then re-run the analysis. The overlapping of the mean effect size confidence

interval gave us confidence to use the whole database for further analysis

4.5 Evidence of heterogeneity

We started by fitting the fixed and random effect model to our dataset (Table 4.2). Given the variability in the methodologies, sample size and other covariates shared by selected studies we hypothesized that a random effect model will be the best for our dataset. The amount of heterogeneity in the true Log response ratio was estimated to $\tau^2 = 0.4678$. The test of heterogeneity showed statistically significant heterogeneity among true Log response ratio ($Q = 98501.9279, df = 1465, P < 0.0001$). Under the random effect model, the estimated average Log response ratio was equal to $\hat{R} = -0.3829$ ($95\% CI : -0.4229$ to $- 0.3428$). The results suggest that the increase of ambient temperature affect negatively on different species in general at a rate of 30%. The null hypothesis $R = 0$ was rejected ($Z = -18.7492, P < 0.0001$). However, note that the overall response ratio under the fixed effect model was $-0.258, SE = 0.002$. The overall R under the random effect model was -0.383 with the standard deviation of 0.02, which is statistically significant ($Z = -18.75, P < 0.0001$) (Table 4.2) . This means that the response ratio is 0.681813 with 95% confidence interval from 0.655079 to 0.709638.

Table 4.2: Effect of temperature rise on biodiversity using Fixed and Random effect models. ES: effect size, SE: Standard Deviation, LL: Lower Limit, UL: Upper Limit

Model	Effect size and 95%CI					Test of null (2-Tail)		Heterogeneity			
Model	**N**	**ES**	**SE**	**LL**	**UL**	**Z-value**	**P-value**	**Q-value**	**df**	**P-value**	**I-squared**
Fixed	1466	-0.258	0.002	-0.262	-0.253	-122.67	< 0.0001	98504.5	1465	< 0.0001	98.5
Random	1466	-0.383	0.02	-0.423	-0.343	-18.75	< 0.0001				

Classifying our main dataset in two groups of animals and plants, these groups were not evenly affected by ambient temperature change. The animals are more affected by the change of ambient temperature with response ratio of 0.66699 (95% CI:-0.4068, 1.7407). However, plants were affected on response ratio of 0.792154 (95% CI: -0.22917, 1.813478).

Table 4.3: Effect of ambient temperature change on animals and plants species

Model		Log response ratio		Test of null		Heterogeneity			
Group	N	Point estimate	SE	z-value	P-value	Q-value	Df	P-value	I-squares
Animals	819	-0.3968	0.0404	-9.8182	< 0.0001				
Plants	1043	-0.3813	0.0265	-14.4122	< 0.0001				
Test of moderators	1862					304.11	2	< 0.0001	98.40%

4.5.1 Meta regression on taxonomic groups classification

Running a mixed effect model on defined classification within the animal group, the class of birds showed to be more affected than others ($R = -1.1346, SE = 0.04$). In this group of animals, the class of reptiles followed with the Log response ratio of $-0.4974, SE = 0.077$ and the mammals with the Log response ratio of $-0.231, SE = 0.044$. However, the effect of temperature change on insects showed to be not significant $P = 0.0834$.

Within the group of plants, angiosperms were negatively affected with ambient temperature change ($R = -0.104, SE = 0.002$). The effect on ferns, moss and algae showed to be not statistically significant (see Table 4.4). The class of gymnosperms showed to be negatively affected by the change of temperature with $R = -0.124, SE = 0.064$.

Table 4.4: The effect of temperature rise on species taxa

Groups		**Effect size**		**Test of null**		**Heterogeneity**		
Groups	N	Point estimate	SE	Z-value	P-value	Q-value	Df	P-value
Random effect analysis								
Algae	1	-1.3291	0. 8733	-1.51	0.128			
Amphibians	53	-0.772	0.076	-10.122	< 0.0001			
Angiosperms	303	-0.10386	0.0021	-49.495	< 0.0001			
Birds	207	-1.1346	0.0389	-29.15	< 0.0001			
Insects	248	-0.059	0.03	15.889	0.0834			
Ferns	2	0.1631	0.3783	0.4312	0.6663			
Fungi	65	-0.051	0.1112	-0.4585	0.6466			
Gymnosperms	64	-0.1235	0.064	-15.889	< 0.0001			
Mammals	28	-0.231	0.1438	-1.6103	< 0.0001			
Moss	82	0.0183	0.1027	0.1797	0.8574			
Reptiles	51	-0.4974	0.077	-6.459	< 0.0001			
Test of moderators						997.6	12	< 0.0001

4.5.2 Meta regression on location where the study was carried out.

We carried on with a mixed effect model with respect to the location where the study has been carried out. The species groups respond individually with respect to the location. The studies carried on Australia showed that this location is highly negatively affected by temperature change ($R = -0.901, SE = 0.111$). On the other hand, biodiversity within African continent was negatively effected by temperature increase among others ($R = -0.398, SE = 0.085$). Some marine species are not significantly affected by this change of ambient temperature (Table 4.5).

Table 4.5: Prone regions to the increase of temperature

Groups		Effect size		Test of null		Heterogeneity		
Group	N	ES	SE	z-value	P-value	Q-value	Df	P-value
Mixed effect model								
Africa	154	-0.3983	0.0848	-4.69	< 0.0001			
Australia	68	-0.9014	0.1113	-8.0976	< 0.0001			
Asia	48	-0.3031	0.1048	-2.8929	0.0038			
North America	930	-0.0821	0.0389	-2.1078	0.035			
South America	121	-0.3060	0.0651	-4.7039	0.0001			
Eurasia	63	-1.6766	0.0820	-20.446	< 0.0001			
Europe, Asia and Africa	4	-0.24	0.2965	-0.8095	0.4182			
Antarctica	4	-0.2183	1.7453	-0.1261	0.9005			
Indian Ocean	3	-1.45	0.3863	-3.7541	0.0002			
Pacific Ocean	18	-0.344	0.3337	-1.0319	0.3021			
Worldwide	22	0.0812	0.223	0.3641	0.7158			
Total heterogeneity Test of moderators						768.43	13	< 0.0001

4.5.3 Meta regression on methodology

The mixed effect model with respect to methodology (observation vs modelling studies) showed that the modelling studies had a high negative significant effect (R = -0.49, SE=0.023, P < 0.0001) relative to observation studies. However, the effect size with respect to the observation studies was not statistically significant (R= -0.059, SE= 0.04, P = 0.14). Among different models used in modelling studies, BIOMOD models had the highest effect magnitude and the general linear models with the smallest effect of ambient temperature change (Appendix B.1). From the result of the simulation studies, we speculate that the models used to estimate the effect of temperature on species exaggerate the reality found in the observations studies.

Table 4.6: Effect of temperature rise on observations and simulations.

Groups		**Effect size**		**Test of null**		**Heterogeneity**		
Group	N	ES	SE	Z-value	P-value	Q-val	Df	P-value
Mixed effect analysis								
Observation	510	-0.0592	0.0401	-1.478	0.14			
Simulation	1567	-0.49	0.0227	-21.57	< 0.0001			
Total between						467.33	2	< 0.0001

4.5.4 Meta regression on species attributes

During the process of collecting the data, the effect of temperature change was assessed with respect to biomass, species richness, density change within population and suitable habitat. Running a meta regression model with respect to these moderators, the species richness was highly affected by temperature ($R = -0.448, SE = 0.076$) followed by suitable habitat ($R = -0.331, SE = 0.032$). However, the effect with respect to the two other categories showed to be not statistically significant. This shows that main species attributes in determining the effect of ambient temperature change on biodiversity are species density and species habitat.

Table 4.7: Effect of temperature rise on species attributes

Groups		Effect size		Test of null		Heterogeneity		
Mixed effect model								
Group	N	Estimate	SE	Z-value	P-value	Q-value	Df	P-value
Biomass	49	0.0128	0.14	0.092	0.93			
Density change	45	0.2054	0.126	1.64	0.103			
Suitable habitat	781	-0.3313	0.0317	-10.46	< 0.0001			
Species richness	128	-0.4484	0.0756	-5.93	< 0.0001			
Test of moderators						147.21	4	<0.0001

4.5.5 Meta regression analysis on species dispersal capacity

As observed during the process of collecting the data, we raised the question regarding the consistency in considering two different scenarios related to the species dispersal capacity in estimating the effect of ambient temperature on different species. Some cases (1051) in our database considered the information of natural dispersal in assessing the effect of ambient temperature change on

a specie of interest. However, some cases did not provide the information considering dispersal capacity. We classified our database in two parts where a group called "With" which consist of studies considering that variable and a group called "Without" which consist of studies which did not consider the variable. We were interested by the importance of considering this variable in estimating the impact of climate change. We proceeded with a mixed effect model with respect to the aforementioned two groups and we tested for the difference between the two overall effect size of the two groups (Figure 4.2).

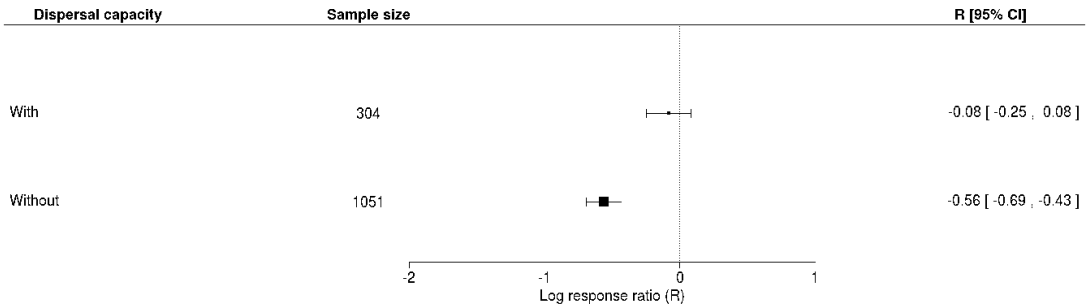

Figure 4.2: Effect of dispersal capacity on species response to temperature rise

On the overall of our dataset, 304 cases considered species dispersal capacity in their methodology when assessing the effect of temperature. However, 1051, did not consider it. We found that the overall effect size of current and predicted temperature when considering the species dispersal was not statistically significant (R = -0.079, P = 0.0615). On the other hand, the overall Log response ratio on cases which did not consider the species dispersal capacity, was highly negative ($R = -0.548, SE = 0.026$). The null test showed that the overall Log response ratio reported by this category was statistically significant ($Z = -21.11, P < 0.0001$). Furthermore, the mean test comparison for these two groups showed that they were statistically different ($Q = 449.54, df = 2, P < 0.0001$).

4.5.6 Meta regression analysis on studies within tropics

We also classified our dataset into two categories: tropics and extra tropical areas. Tropics included all studies whose full or more that half of their geographical extent was within the tropic of Cancer and tropic of Capricorn. Otherwise, it was classified within extra tropical areas. The results show a negative significant effect size in both lower and higher latitudes. The test

for null hypothesis ($R_1 = R_2$) show that they were significantly different ($Q = 346.41; P < 0.0001$). This support the negative impact of observed climate change outside the tropics (Table 4.8).

Table 4.8: Effect of temperature rise on species within and outside tropics

Groups		Effect size		Test of null		Heterogeneity		
Mixed effect analysis								
Groups	N	Estimate	SE	Z-value	P-value	Q-value	df	P-value
In tropics	275	-0.3421	0.0559	-6.1221	< 0.0001			
Out tropics	1753	-0.3894	0.0222	-17.5764	< 0.0001			
Test of moderators						346.41	2	< 0.0001

We know that species at low altitude will be more affected by temperature change than species in high altitude. From this, we expected that the effect of temperature to decline as we increase altitude. However, we found that at low altitudes, some species will suffer from temperature change and others will benefit from it. Furthermore, at higher altitude (800 m), many species will not cope the change in ambient temperature (Figure 4.3).

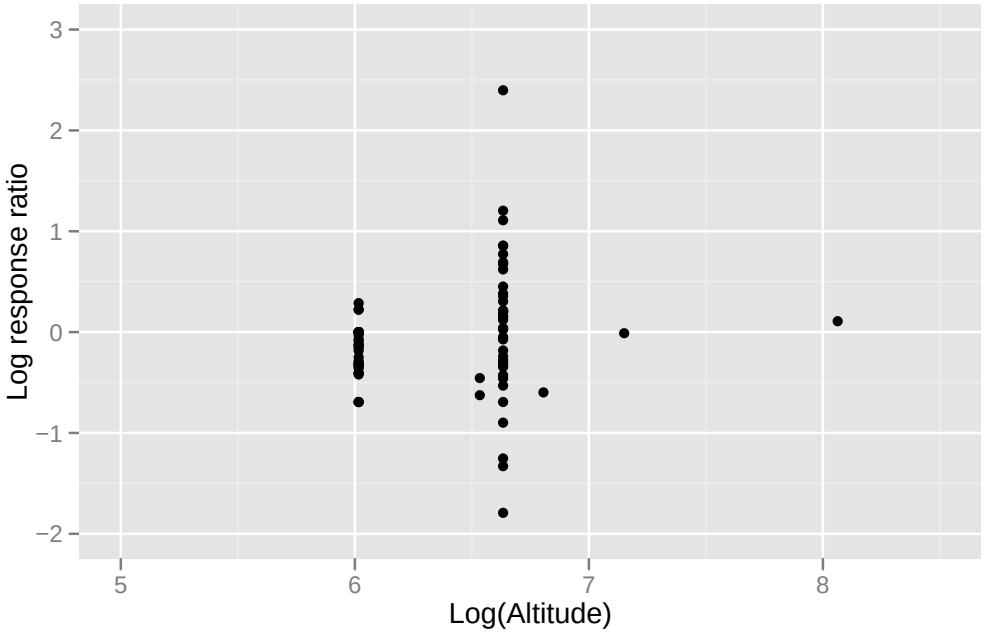

Figure 4.3: The relationship between Log transformed altitude (in meters) and the effect of ambient temperature change

4.6 Mixed effect analysis on geography extent

We subdivided the dataset with respect to geographic extent of the studies. We subdivided all effect size in four categories. The cardinal of each category was equal. We achieved this from the quartiles analysis. The first category was formed by cases having the geographic extent varying from 0 to 100 km^2. The second category was formed of cases having the geographic extent within 100 - 256 km^2. The third category was formed by the cases corresponding to geographic extent varying between 256 and 6183 km^2; and the last category was formed by cases corresponding to geographic extent varying between 6183 and 1237000 km^2.

Table 4.9: Effect of temperature rise on study geographic extent

Groups		Log response ratio		Test of null		Heterogeneity		
Mixed effect model								
Group	N	Point estimate	SE	Z-value	P-value	Q-value	df	P-value
< 100		-0.4982	0.0465	-10.7027	< 0.0001			
$100 < x \leq 256$		-0.8018	0.0417	-19.2423	< 0.0001			
$256 < x \leq 6183$		-0.0811	0.0414	-1.9587	0.0502			
$x > 6183$		-0.3409	0.0517	-6.5897	< 0.0001			
Test of moderators						540.444	4	< 0.0001

The higher statistically significant effect size was reported in the second category ($R = -0.8, SE = 0.04$). However, the effect size reported by the third category was not statistically significant (P = 0.0502). Furthermore, the null hypothesis analysis ($R_1 = R_2 = R_3 = R_4$) was rejected ($Q = 540.45, df = 2, P < 0.0001$)

4.7 Discussion

The aim of this study was to assess whether the current theory of the negative impact of temperature change on biodiversity was supported by empirical studies. Our analysis was based on a standardized literature analysis across animals and plants within terrestrial and aquatic habitats. We subdivided cases extracted from the published articles in different classes. We measured the effect with respect to four biodiversity measures: species richness, suitable habitat, species biomass and species density change.

In order to investigate the aim of this study, we construct a real dataset of different species response to ambient temperature change. From defined

terms, we collected 99 published articles from which 2077 cases have been extracted. The same methodology has been used by other meta-analysis work [e.g. Vila *et al.*, 2011]. However, in the work of Harrison [2011], they insisted on the importance of incorporating unpublished data. In this work, we only considered published articles (data). Temperature is the most significant climatic variable as many organism's metabolic processes (e.g. photosynthesis, respiration and growth rate) are temperature dependent. According to Van't Hoff's law, which state that the logarithm at which these processes take place is proportionally to the temperature at which it is taking place. Furthermore, the physiological processes are promoted by enzymes and proteins which in general are not active at high temperature [Ford, 1982]. This may be the explanation why the increase of ambient temperature is deleterious to most of the organism which are not adapted to new environment conditions.

Overall, empirical data support the theory that ambient temperature change is negatively affecting biodiversity. Both classes of animals and plants showed to negatively respond to this change. Our results showed to be in the same direction as the results of Maclean and Wilson [2011].

Considering the main division of our dataset, the class of animals showed to be highly affected by the change of temperature relatively to the class of plants. This was contrary to our expectation due to this reason: Given the theory of higher dispersal capacity of animals (e.g. birds) to new geographical areas with favorable environment condition relatively to plants.

The overall effect size reported by the observations studies was not statistically significant. This may partially be explained by the fact that most of the current observation studies are based on data collected on short interval of time because the data on long period of time are difficulty to compile and most of the time very expensive. However, the overall effect size reported by prediction cases were statistically significant. To our knowledge, these studies were based on long term data. This means that the predicted temperature change is a threat to the most species and may increase their probability of extinction, meaning decline in ecosystem biodiversity. Furthermore, based on the biotic resistance hypothesis, which states that ecosystems with high biodiversity are more robust to invaders compared to ecosystems with low biodiversity [Jeschke *et al.*, 2012], we may speculate that increase in temperature may be a catalyst in some ecosystems for biology invasion.

The analysis of empirical studies showed that current studies assessing

the impact of temperature change on biodiversity are somehow biased toward higher plants than lower plants (e.g. algae, fungi) (Table 4.4). We found that several cases included in our dataset were not negatively affected by the rise of temperature. This may partially be explained by the fact that the life state of these depend on their degree of hydration which is proportionally to the humidity of surrounding air rather that temperature [Ford, 1982].

Considering the tolerance limit, each species of plants and animals has its critical threshold value limit to the change of temperature. The most effective way to understand this phenomenon, will be through the species behaviour-temperature manipulation. However, this was not in the scope of this study. Furthermore, the published studies showed that in overall, the considered species in our dataset start to respond negatively to ambient temperature increment when it is above 4 ℃on average (Figure 4.4).

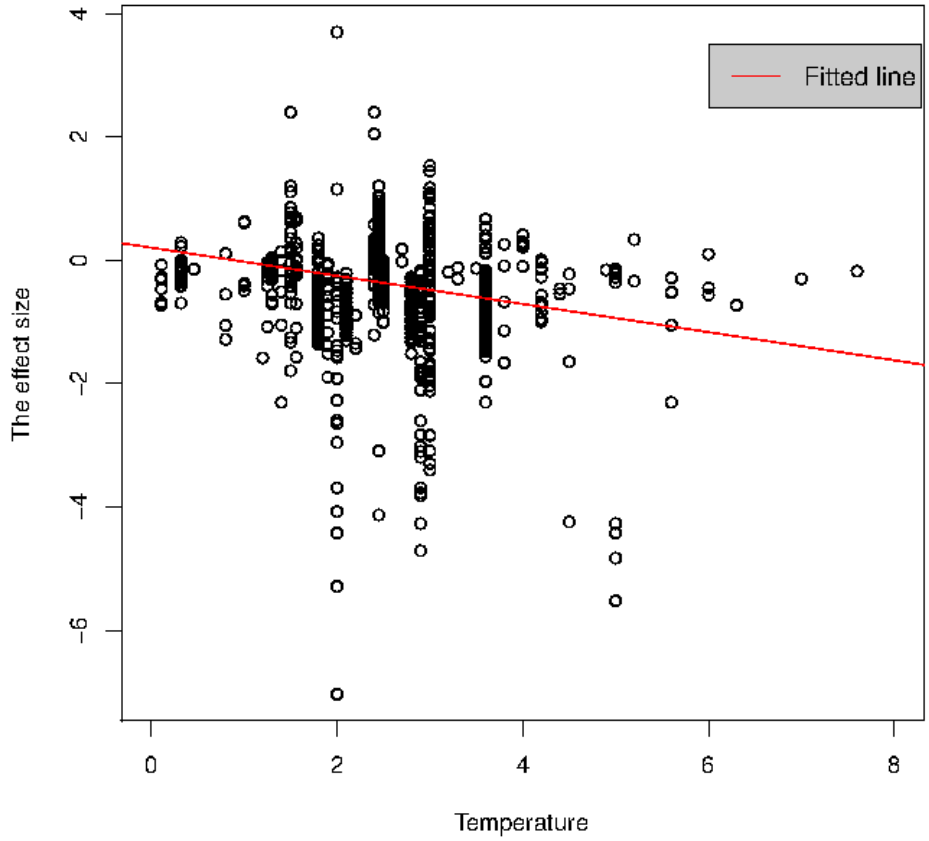

Figure 4.4: The relationship between temperature (T) increment (in ℃) and the effect size (R) of species response. Red line represents a fitted linear model of equation R = 0.728 - 0.164 T

In conservation process, more studies use the direct biodiversity measures (e.g. species richness, population density). Among these measures, some were sensitive to the change of temperature, however, others were not. We find that the species richness and suitable habitat were the most sensitive to the ambient temperature change (Table 4.7). This indicates that suitable habitat and species richness are good measures of species response within a community to the ambient temperature change.

Most methods used to assess the impact of climate change are sensitive to geographical extent and elevation range [Randin *et al.*, 2009]. From the results, the overall range of effect size was independent from the geographical extent of the study (Table 4.9). On the other hand, regarding the elevation extent, we found a statistical significant effect size in both low and high elevation range.

Chapter 5

Conclusion

The present work was done to provide a general overview from published articles assessing the impact of climate change on biodiversity. We only considered the most important climatic factor, temperature change. The result and discussion presented in the previous chapter are based on the meta-analysis approach applied to real data set collected from published articles. We fitted this real data set to the random effect model with and without moderators using classical procedures of fitting general linear models.

Climate change is now thought to have an impact over longer periods than previously believed and the impacts on biodiversity will vary depending on the organism considered and the spatial scale evaluated. While experimental studies manipulate some variables and evaluate the effect on a limited number of organisms, the simulation studies find associations under predicted scenarios. A meta-analysis approach is sensitive enough to compile and summarize the species response across different scales and locations.

We found that in overall, species are negatively affected by the temperature change. Among four species attributes considered in study, species richness and species range richness were the more sensitive to the change of temperature. Contrary to general believe that species will shift to high altitude for suitable habitat, we found that these high altitude regions may not be suitable. Models currently used in estimating the effect of climate change may overestimate the reality found in observations studies. Species with high dispersal capacity will be less affected by change in temperature.

5.1 Future research

In this work, we tested different hypotheses on the impact of ambient temperature change on species richness, suitable habitat,biomass and species abundance. Even when temperature is the most important climatic factor in biological terms, there are others variables of climate which are important to the biology of organisms, such as precipitation, ocean acidity and oxygen level. A study of the assessment of species response by considering more climatic variables will add valuable information in order to comprehend fully diverse ways in which different species respond to climate change. We therefore recommend further research be undertaken considering aforementioned details.

Appendices

Appendix A

List of published articles used in meta-analysis

Table A.1: List of published articles from which the data have been extracted from.

Number	Papers	Number of cases
1	McClean *et al.* [2011]	3
2	Menendez *et al.* [2006]	3
3	Fonty *et al.* [2009]	34
4	Thuiller *et al.* [2005]	8
5	Thomas *et al.* [2004]	50
6	Hu and Jiang [2011]	12
7	Araújo *et al.* [2011]	236
9	Midgley *et al.* [2003]	56
10	Kreyling *et al.* [2010]	25
11	Bakkenes *et al.* [2002]	12
12	Kissling *et al.* [2010]	4
13	Thuiller *et al.* [2006]	13
14	Sommer *et al.* [2010]	8
15	Randin *et al.* [2009]	4
16	Pompe *et al.* [2008]	9
17	Kueppers *et al.* [2005]	4
18	Schwartz *et al.* [2006]	2

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Table A.1 –*Continued from previous page*

Number	Papers	Number of cases
19	III *et al.* [1995]	15
20	Calef *et al.* [2005]	13
21	Parton *et al.* [1995]	14
22	Kardol *et al.* [2010]	56
23	Yang *et al.* [2011]	7
24	Rodenhouse *et al.* [2008]	300
25	Muhlfeld *et al.* [2011]	2
26	Koleček *et al.* [2010]	12
27	Burgmer and Hillebrand [2011]	1
28	Cameron and Scheel [2001]	113
29	Koontz *et al.* [2001]	2
30	Dietterick *et al.* [1999]	6
31	Bokhorst *et al.* [2011]	3
32	Wilmking *et al.* [2006]	1
33	Luoto and Heikkinen [2007]	200
34	Feeley and Silman [2010]	5
35	Li *et al.* [2008]	30
36	Ohlemüller *et al.* [2006]	2
37	Britton *et al.* [2009]	3
38	Cabeza *et al.* [2010]	1
39	Lehmann *et al.* [2010]	2
40	Matter *et al.* [2011]	8
41	Engler *et al.* [2011]	21
42	Hudson and Henry [2010]	20
43	Molau [2010]	1
44	Bokhorst *et al.* [2009]	1
45	Stenström *et al.* [1997]	1
46	Barrett *et al.* [2008]	10
47	Both *et al.* [2006]	1
48	Chen *et al.* [2009]	6
49	Davies *et al.* [2005]	1
50	Field *et al.* [2006]	1

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Table A.1 –*Continued from previous page*

Number	Papers	Number of cases
51	Graham *et al.* [2006]	3
52	Hörnfeldt *et al.* [2005]	1
53	Jenouvrier *et al.* [2005]	3
54	Kausrud *et al.* [2008]	1
55	Kausrud *et al.* [2007]	1
56	Lovvorn *et al.* [2009]	1
57	Mceachern *et al.* [2009]	2
58	McMenamin *et al.* [2008]	3
59	Mueter and Litzow [2008]	1
60	Pauli *et al.* [2006]	21
61	Murphy *et al.* [2007]	1
62	Pfeifer *et al.* [2006]	1
63	Rolland *et al.* [2008]	1
64	Rolland *et al.* [2009]	2
65	Ruhl *et al.* [2008]	4
66	Vargas *et al.* [2006]	1
67	Waite and Strickland [2006]	1
68	Wallisdevries and Van Swaay [2006]	1
69	Gómez-Mendoza and Arriaga [2007]	68
70	Thuiller [2003]	1
71	Lemoine *et al.* [2007]	2
72	Baskett *et al.* [2009]	1
73	Montes-Hugo *et al.* [2009]	1
74	Marchand *et al.* [2004]	1
75	Wahren *et al.* [2005]	26
76	Hollister *et al.* [2005]	219
77	Franco *et al.* [2006]	4
78	Marchand *et al.* [2006]	1
79	Weatherhead [2005]	1
80	Virkkala *et al.* [2008]	62
81	Attorre *et al.* [2007]	1
82	Ellis *et al.* [2007]	2

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Table A.1 –*Continued from previous page*

Number	Papers	Number of cases
83	Hughes *et al.* [2008]	8
84	Marrero-Gómez *et al.* [2007]	1
85	Shoo *et al.* [2005]	12
86	Newsham and Garstecki [2007]	6
87	Ludwig *et al.* [2006]	1
88	Mølgaard and Christensen [1997]	5
89	Jensen *et al.* [2008]	3
90	Logan *et al.* [2007]	1
91	Jarema *et al.* [2009]	2
92	Goulson *et al.* [2005]	18
93	Patricio and Esther [2008]	3
94	ÓNeill *et al.* [2008]	33
95	Gedan and Bertness [2009]	3
96	Reif *et al.* [2008]	1
97	Vargas *et al.* [2008]	2
98	Maschinski *et al.* [2006]	2
99	Malcolm *et al.* [2006]	200

Appendix B

Effect of temperature change on simulation models

Table B.1: The effect of temperature change on simulations models. NLMEM stands for non-linear models

Groups		**Effect size**		**Test of null**		**Heterogeneity**		
Mixed effect model								
Groups	**N**	**Estimate**	**SD**	**z-value**	**p-val**	**Q-value**	**DF**	**p-val**
BIOMOD	269	-0.8267	0.0336	-24.62	< 0.0001			
Budget models	2	0.0006	0.3884	0.0016	0.9988			
Digital elevation model	25	-0.4571	0.1758	-2.5995	0.0093			
General additive model	286	-0.4054	0.0353	-11.4794	< 0.0001			
General least square model	24	0.1181	0.1132	1.0432	0.2969			
Maxent	15	-0.3269	0.1732	-1.8874	0.0591			
General Linear Model	175	-0.1912	0.0655	-2.9177	0.0035			
Species Distribution Model	9	-0.2510	0.3903	-0.6431	0.5201			
NLMEM	33	0.0307	0.143	0.2147	0.83			
Global vegetation Model	200	-0.3644	0.046	-7.93	< 0.0001			
Random Forest	3	-0.7733	0.3168	-2.4408	0.0147			
Test of moderators						828.06	12	< 0.0001

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